Package: CardiacDP (via r-universe)

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Title Automated Cardiac Data Processing via ACF, GA & Tracking Index

Version 0.4.3

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Description An algorithm developed to efficiently and accurately process complex and variable cardiac data with three key features: 1. employing autocorrelation to identify recurrent heartbeats and use their periods to compute heart rates; 2. incorporating a genetic algorithm framework to minimize data loss due to noise interference and accommodate within-sequence variations; and 3. introducing a tracking index as a moving reference to reduce errors. Lau, Wong, & Gu (2026) <https://ssrn.com/abstract=5153081>.

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Roxygen list(markdown = TRUE)

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Depends R (>= 4.3.0)

Imports data.table, doParallel, dplyr, foreach, ggplot2, purrr, RColorBrewer, stringr

Suggests testthat (>= 3.0.0)

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`collatedata` *CardiacDP - collatedata()*

Description

Automatically read and collate separate .csv files in chronological order as inferred by the file names and in hierarchy.

Usage

```
collatedata(file_path, output_file = NULL, verbose = FALSE)
```

Arguments

`file_path`	Designate the path to your file, must be a .zip file
`output_file`	Optional path to write the collated data table as a CSV file. May be either a full file path (e.g. `/path/to/out.csv`) or an output directory (e.g. `/path/to/outdir`). If a directory (or a path without a file extension) is provided, a file named `<input_stem>_collated.csv` is written inside it. Default NULL (no file written).
`verbose`	Logical; if TRUE, emit progress messages. Default FALSE.

Value

A single collated data table

Examples

```
zip_path <- system.file("extdata", "example.zip", package = "CardiacDP")
collated <- collatedata(zip_path)
```

`computeHR` *CardiacDP - computeHR()*

Description

Employing the autocorrelation function (ACF) with a genetic algorithm framework to locate periodic sub-sequences within each sequence. From the candidate heart rates of these sub-sequences, the final results are either evaluated based on the autocorrelation value or a tracking index (TI).

Usage

```
computeHR(
  file_path,
  reduce_res = 0.01,
  pop_size = 10L,
  max_gen = 20L,
  patience = 2L,
  an_in = 1,
  acf_thres = 0.5,
  lr_thres = 0.7,
  ncore = NULL,
  output_dir = NULL,
  save_outputs = FALSE,
  verbose = FALSE
)
```

Arguments

file_path	Designate the path to your file, must be a .zip or .csv file
reduce_res	Time interval of reduced resolution (seconds), by default 0.01
pop_size	Number of populations used in the genetic algorithm, by default 10L
max_gen	Maximum number of generations in the genetic algorithm, by default 20L
patience	Patience threshold (maximum number of generations with no further changes) in the genetic algorithm, by default 2L
an_in	Analysis interval (length of a sequence; in minute), by default 1
acf_thres	Threshold used in ACF to classify periodic oscillations from aperiodic noises, by default 0.5
lr_thres	Linear regression r-sq threshold in extrapolating the tracking index, by default 0.7
ncore	Integer; number of CPU cores to use for the genetic algorithm. If NULL (default), uses `parallel::detectCores() - 1`. During `R CMD check`, cores are clamped to a small number to satisfy check limits.
output_dir	Optional directory to write CSV/PNG outputs when `save_outputs = TRUE`. If NULL, defaults to `tempdir()`.
save_outputs	Logical; if TRUE, write CSV/PNG outputs to `output_dir`. Default FALSE.
verbose	Logical; if TRUE, emit progress messages. Default FALSE.

Value

The positions (in indices) and durations of the sub-sequences (finalsubseq) and the corresponding candidate HR (candidateHR) obtained from the genetic algorithm, and the final results evaluating the candidates by autocorrelation values (results_ACF) or the tracking index (results_TI), which contains the details of the subsequences after checking for resolution (subseqHR with Time_min column), the weighted heart rate per sequence (weightedHR with Time_min column) and a plot (plot). If `save_outputs = TRUE`, file paths are recorded in `output$files`.

Examples

```
# use the default parameters to analyse a zip file
# the collatedata function will be called automatically
zip_path <- system.file("extdata", "example.zip", package = "CardiacDP")
computeHR(file_path = zip_path, save_outputs = FALSE)



# use the default parameters to analyse a csv file
csv_path <- system.file("extdata", "example.csv", package = "CardiacDP")
computeHR(file_path = csv_path, reduce_res = 0.1,
          save_outputs = FALSE)



# use customized parameters to analyse a zip file
zip_path <- system.file("extdata", "example.zip", package = "CardiacDP")
computeHR(zip_path, reduce_res = 0.1, max_gen = 30L,
          lr_thres = 0.8, save_outputs = FALSE)



# use custom parameters to analyse a csv file
csv_path <- system.file("extdata", "example.csv", package = "CardiacDP")
computeHR(csv_path, reduce_res = 0.1, pop_size = 20L,
          an_in = 1, acf_thres = 0.6, save_outputs = FALSE)
```

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